

```
GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:      August 30, 2001, 20:37:17 ; Search time 1583.92 Seconds
              (without alignments)
              3735.975 Million cell updates/sec

Title:       US-09-691-763B-4
Perfect score: 626
Sequence:    1 agcgcttttctgagggc.....ggaagggaaggatcactt 626

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:    10228115 seqs, 4726426750 residues                20456230

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :
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115: gb_est46.*
116: gb_est47.*
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9709 row: e column: 23
High quality sequence stop: 659.

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3904126"
/clone_lib="NIH_MGC_70"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."
BASE COUNT 217 a 236 c 281 g 154 t
ORIGIN

Query Match 41.4%; Score 259; DB 141; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 172 gagccatcttgatgcgctggagaaacctgacccgagggagctcaagaagttcaagctg 231
Db 1 GAGCGCATCTGGATGGCGCTGGAGAACCTGACCGCGGAGAGCTCAAGAAGTTCAAGCTG 60
Qy 232 aagctgctgcgtgcgctgcgagggctacggcgctcccgcgggcgcgctgctg 291
Db 61 AAGCTGCTGCTGGCTGGCGGAGGCTACGGGCGCATCCCGCGGGCGCGCTGCTG 120
Qy 292 tcatgagccttgacacctacacgaagctggctcagctctctacctggagacacctacggc 351
Db 121 TCCATGGAGCGCTTGGACCTCAGCGACAAGCTGGTCAAGCTTCTTACCTGGAGACCTACGCG 180
Qy 352 gccagctcaccgctaacgtgctgcgcacatggcgctgcaggagatggccggcgagctg 411
Db 181 GCCGAGCTCAGCGCTAAGTGTGCGGACATGGGCTGCAGGAGATGGCGGGCAGCTG 240
Qy 412 caggcgccacgacccagg 430
Db 241 CAGCGCGCCACGCCACGAG 259

RESULT 7
BE908204
LOCUS A1148558 678 bp mRNA EST 28-OCT-1998
DEFINITION qc68g10.x1 Soares.placenta.8to9weeks.2NBP8to9w Homo sapiens CDNA clone IMAGE:1714818 3' similar to TR:O15553 O15553 PYRIN. ;, mRNA sequence.
ACCESSION A1148558
VERSION A1148558.1 GI:3677027
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 678)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 804 Std Error: 0.00
Seq primer: -40m13 fwd. ER from Amersham
High quality sequence stop: 402.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1714818"
/clone_lib="Soares.placenta.8to9weeks.2NBP8to9w"
/dev_stage="two placenta; one from 8 weeks and another from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGGATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Facima Bonaldo."
BASE COUNT 114 a 202 c 217 g 145 t
ORIGIN

Query Match 41.3%; Score 258.4; DB 16; Length 678;
Best Local Similarity 99.6%; Pred. No. 2.1e-42;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 172 gagccatcttgatgcgctggagaaacctgacccgagggagctcaagaagttcaagctg 231
Db 678 GACCCCATCTGGATGGCGCTGGAGAACCTGCCCGCGGAGAGCTCAAGAAGTTCAAGCTG 619
Qy 232 aagctgctgcgtgcgctgcgagggctacggcgctcccgcgggcgcgctgctg 291
Db 618 AAGCTGCTGCTGGCTGGCGGAGGCTACGGGCGCATCCCGCGGGCGCGCTGCTG 559
Qy 292 tcatgagccttgacacctacacgaagctggctcagctctctacctggagacacctacggc 351
Db 558 TCCATGGAGCGCTTGGACCTCAGCGACAAGCTGGTCAAGCTTCTTACCTGGAGACCTACGCG 499
Qy 352 gccagctcaccgctaacgtgctgcgcacatggcgctgcaggagatggccggcgagctg 411
Db 498 GCCGAGCTCAGCGCTAAGTGTGCGGACATGGGCTGCAGGAGATGGCGGGCAGCTG 439
Qy 412 caggcgccacgacccagg 431
Db 438 CAGCGCGCCACGCCACGAGG 419

RESULT 8
BE908204
LOCUS BE908204 675 bp mRNA EST 20-OCT-2000
DEFINITION 601500461F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902319 5', mRNA sequence.
ACCESSION BE908204
VERSION BE908204.1 GI:10402543
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 675)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM9704 row: j column: 16
 High quality sequence stop: 660.

FEATURES

source
 1. .675
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3902319"
 /clone_lib="NIH_MGC_70"
 /tissue_type="epithelioid carcinoma"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."
 BASE COUNT 151 a 214 c 198 g 112 t

ORIGIN

Query Match 39.5%; Score 247; DB 141; Length 675;
 Best Local Similarity 100.0%; Pred. No. 4.1e-40;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 185 atgcgtgagaaacctgaccgcgagagagctcaagaagtcaagctgaagctgctcgg 244
 Db 1 ATCCGCTGAGAACTGACCCCGGAGAGCTCAAGAACTTCAAGCTGAAGCTGTCGG 60
 Qy 245 tgcgcgtgcgagaggtacagcgccatcccgcgcgctgctgtccatgagcgct 304
 Db 61 TGGCGGTGGCGAGGGCTACGGGCGCATCCCGGGGGCGCTGCTGCCATGACGCT 120
 Qy 305 tggacacaccgagaaagctgctgaagcttacctgagacacacagcgagctcaacg 364
 Db 121 TGGACCTACCCAGCAAGCTGGTCAAGTCTTACCTGGAGACCTACGGCGCGAGCTCACCG 180
 Qy 365 ctacacgtgctgcgacatggcctgcaggagatggcgggcgagctgcgagcgccacgc 424
 Db 181 CTAACGTGTCGGCGACATGGCTTGCGAGAGATGGCGGGGCGCTGCAGGCGCCACGC 240
 Qy 425 accaggg 431
 Db 241 ACCAGGG 247

RESULT 9

AI346818 615 bp mRNA EST 02-FEB-1999
 LOCUS gp58f05.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1927233 3'
 DEFINITION similar to TR:015553 015553 PYRIN. ; mRNA sequence.
 AI346818
 ACCESSION AI346818.1 GI:4084024
 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 615)

REFERENCE

1 (bases 1 to 615)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)

AUTHORS

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio-llnl.gov/bbrp/image/image.html](http://bio-llnl.gov/bbrp/image/image.html)
 Insert Length: 751 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 457.

FEATURES

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 1. .615
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1927233"
 /clone_lib="NCI_CGAP_C08"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 108 a 182 c 193 g 132 t

ORIGIN

Query Match 39.0%; Score 244.4; DB 19; Length 615;
 Best Local Similarity 97.4%; Pred. No. 1.4e-39;
 Matches 259; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
 Qy 172 gacgccatcttgatgcgtgagaaacctgaccgcgagagagctcaagaagtcaagctg 231
 Db 615 GACGCCATCTTGGATCGCTGGAGAACCTGACCCCGGAGAGCTCAAGAACTTCAAGCTG 556
 Qy 232 aagctgctgctgcgtgcgcgtgcgcgagggctacggcgccatcccgcgggcgcgctgctg 291
 Db 555 AAGCTGCTGTCGGTGGCGCTGCGCGAGGGCTACGGCGGCATCCCGCGGGCGCGTGTG 496
 Qy 292 tccatgagccttgagctaccctaccgacaagctggctcagcttacctggagacctacggc 351
 Db 495 TCCATGGACGCTTGGACCTCACCGACAAAGCTTGTTCAGCTTCTACCTGGAGACCTACGGC 436
 Qy 352 ccagagctcaccgtaacgtgctgcgcacatgggctgcagagatggcgcgagctg 411
 Db 435 GCCGAGCTCACCGCTAACGTGCTGCGGACATGGGCTGCAGGAGATGGCGGGCACTG 376
 Qy 412 caggcgg-ccagcaccacagggtgagc 436
 Db 375 CAAGCGGCCACGACCCAGGGCTGC 350

RESULT 10

AI346818 308 bp mRNA EST 27-JUN-1995
 LOCUS Y128A06.r1 Soares breast 3NDHBst Homo sapiens cDNA clone
 DEFINITION IMAGE:159538 5', mRNA sequence.
 AI346818
 ACCESSION AI346818.1 GI:880928
 VERSION EST.
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 308)

REFERENCE

1 (bases 1 to 308)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlff, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohldmann, P. and Willson, R.
 The WashU-Werck EST Project
 JOURNAL Unpublished (1995)


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mRNA sequence.
BE560228
VERSION BE560228.1 GI:9803948
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM356 row: d column: 08
High quality sequence stop: 728.
Location/Qualifiers
1. 830
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3678679"
/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

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BASE COUNT 172 a 237 c 277 g 144 t
ORIGIN

Query Match 35.2%; Score 220.4; DB 137; Length 830;
Best Local Similarity 99.1%; Pred. No. 9e-35;
Matches 232; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 agcgctttgtgagggcaacgacggcgggggggagtcgggagaccagagtgaggag 60
|||||
Db 58 AGCGCCTTTTGTGTGAGGGCAACGGACCGGGGGGGAGTCGGGAGACCAAGTGGGAGG 117
|||||

QY 61 aagcggggagtcacaggttcgcccgagcgagcttcctctgtgctgagcgctgcagcg 120
|||||
Db 118 AAGGC-GGAGTCCAGGTTCGGCCCCCGGAGCCGACTTCTCTGTGTCGGCGGTGCAGCG 176
|||||

QY 121 ggtgagcgagcgagcgcgggggtcctgtgagccatggggcgcgcgagcgccatc 180
|||||
Db 177 GGTGAGCGCGCGGAGCGCGGGGATCCCTGAGCCATGCGCGCGCGCGCGCCGACATC 236
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QY 181 ctgagtcgctggaagaaactgacgcgcgagagagctcaagaagttcaagctgaagctga 234
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Db 237 CTGGATGCTGGAGAACCTGACCGCGGAGGAGCTCAAGAGTTCAAGCTGCAG 290
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RESULT 13
BE560247
LOCUS BE560247 723 bp mRNA EST 15-AUG-2000
DEFINITION 601346055F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678925 5',
mRNA sequence.
ACCESSION BE560247
VERSION BE560247.1 GI:9803967
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

mRNA sequence.
BE560228
VERSION BE560228.1 GI:9803948
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM356 row: d column: 08
High quality sequence stop: 728.
Location/Qualifiers
1. 830
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3678679"
/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT 172 a 237 c 277 g 144 t
ORIGIN

Query Match 34.9%; Score 218.6; DB 137; Length 723;
Best Local Similarity 84.8%; Pred. No. 2.1e-34;
Matches 245; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 agcgctttgtgagggcaacgacggcgggggggagtcgggagaccagagtgaggag 60
|||||
Db 58 AGCGCCTTTTGTGTGAGGGCAACGGACCGGGGGGGAGTCGGGAGACCAAGTGGGAGG 117
|||||

QY 61 aagcggggagtcacaggttcgcccgagcgagcttcctctgtgctgagcgctgcagcg 120
|||||
Db 118 AAGCGGGAGTCCAGGTTCGGCCCCCGGAGCCGACTTCTCTGTGTCGGCGGTGCAGCG 177
|||||

QY 121 ggtgagcgcgagcgcgggggtcctgtgagccatggggcgcgcgagcgccatc 180
|||||
Db 178 GGTGAGCGCGCGGAGCGCGGGATCTGTGAGCCATGCGCGCGCGCGCGCCGACCATC 237
|||||

QY 181 ctgagtcgctggaagaaactgacgcgcgagagagctcaagaagttcaagctgaagctg 240
|||||
Db 238 CTGGATGCTGGAGAACCTGACCGCGGAGGAGCTCAAGAGTTCAAGTGCAGCGGCC 297
|||||

QY 241 tgggtgcgctgcgaggggtacgggcgcatcccgcgggcgcgctgc 289
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Db 298 ACGCACCAGTGGCTCTTGGAGCCCCCGCGCCCAAGAGCTTGGGGCACTCC 346
|||||

RESULT 14
BE564060
LOCUS BE564060 555 bp mRNA EST 25-AUG-2000
DEFINITION BE564060 Bos taurus brain fetus Bos taurus cDNA clone E1BR040C01
5', mRNA sequence.
ACCESSION BE564060
VERSION BE564060.1 GI:9923090
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
```

OM nucleic - nucleic search, using sw model

Run on: August 30, 2001, 20:42:32 ; Search time 39.27 Seconds
(without alignments)
3017.794 Million cell updates/sec

Title: US-09-691-763B-4
Perfect score: 626
Sequence: 1 agcgcctttctgagggc.....ggaaggaaggatcatt 626

Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52.6	8.4	44377	2	US-08-804-227C-7
2	52.6	8.4	44377	2	US-08-804-198-1
3	51.2	8.2	2943	1	US-08-042-747A-7
4	50.8	8.1	30001	1	US-08-125-468-1
5	50.8	8.1	30001	2	US-08-474-933-1
6	50	8.0	2244	1	US-08-476-519-10
7	50	8.0	2244	5	PCT-US95-09323-10
8	50	8.0	2334	1	US-08-476-519-1
9	50	8.0	2334	5	PCT-US95-09323-1
10	49.4	7.9	1765	1	US-08-459-586-15
11	49.4	7.9	1765	2	US-08-282-696-15
12	49.4	7.9	18994	1	US-08-459-586-4
13	49.4	7.9	18994	2	US-08-282-696-4
14	48	7.7	530	3	US-08-758-662-4
15	48	7.7	2310	3	US-09-036-987A-25
16	48	7.7	4524	2	US-08-845-998-7
17	48	7.7	4524	3	US-09-206-537-7
18	47.4	7.6	800	5	PCT-US95-04801-4
19	47.4	7.6	50937	4	US-09-428-517-1
20	46.6	7.4	1656	4	US-09-385-028-14
21	46.6	7.4	1809	1	US-08-455-001-1
22	46.6	7.4	1809	5	PCT-US95-11869-1
23	46.6	7.4	15079	4	US-09-385-028-1
24	46.4	7.4	4188	4	US-07-751-891B-2
25	46.4	7.4	4242	3	US-07-705-490-2
26	46.2	7.4	861	2	US-08-997-080-97
27	46.2	7.4	861	2	US-08-997-362-97

28	46.2	7.4	861	3	US-08-873-970-97
29	46.2	7.4	861	4	US-09-095-855-97
30	46	7.3	1506	4	US-09-158-767-7
31	46	7.3	2261	4	US-09-158-767-1
32	45.8	7.3	11219	1	US-07-642-734C-1
33	45.8	7.3	11219	3	US-08-439-009A-1
34	45.6	7.3	1227	4	US-09-385-028-23
35	45.6	7.3	15079	4	US-09-385-028-1
36	45.2	7.2	4692	2	US-08-916-917-1
37	45.2	7.2	4692	2	US-08-972-631-1
38	45.2	7.2	4692	2	US-08-972-629-1
39	45.2	7.2	4692	2	US-08-972-630-1
40	45.2	7.2	4692	2	US-08-672-211-1
41	45.2	7.2	4692	3	US-09-225-170-1
42	45	7.2	17612	3	US-08-911-853-29
43	45	7.2	17612	4	US-09-479-409-29
44	44.8	7.2	2580	3	US-09-050-863-2
45	44.8	7.2	5452	2	US-09-130-114-1

RESULT 1

US-08-804-227C-7

; Sequence 7, Application US/08804227C

; Patent No. 5876991

; GENERAL INFORMATION:

; APPLICANT: DeHoff, Bradley S.

; APPLICANT: Rostock, Stuart A.

; APPLICANT: Rostock, Paul R., Jr.

; APPLICANT: Sutton, Kimberly L.

; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: THOMAS G. PLANT 1501

; STREET: LILLY CORPORATE CENTER

; CITY: INDIANAPOLIS

; STATE: IN

; COUNTRY: USA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: ASCII(DOS) Text only

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/804.227C

; FILING DATE: February 21, 1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Plant, Thomas, G.

; REGISTRATION NUMBER: 35,784

; REFERENCE/DOCKET NUMBER: X-8231

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317-276-2459

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 44377 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 350..14002

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 14046..20036

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 20110..31284

; FEATURE:

ALIGNMENTS

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,933
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,468
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsevdos, Estelle J
; REGISTRATION NUMBER: 31,145
; REFERENCE/DOCKET NUMBER: 31,255-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3241
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30001 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-933-1

Query Match 8.1%; Score 50.8; DB 2; Length 30001;
Best Local Similarity 45.6%; Pred. No. 0.051;
Matches 219; Conservative 0; Mismatches 257; Indels 4; Gaps 1;

QY 3 cgccttttgcgtgagggcagccgagggcggtgagggagtcgagagcagagtgaggaa 62
Db 24497 CGGCGGCTTCAGAGCGGATGCTGCCGAGCGGAGTGAGCGGGGATGACCCAC 24438
QY 63 ggcgggagtcagagttccgcccgcggagccgacttcctgtgctggcggtcgagcg 122
Db 24437 GTCTGGTGAGACGGGATCGGC----GTGGTGACCGAAGCGGTGGGGCGTTCGGGAGTA 24382
QY 123 gtgagcgcgagcgagcggtgagtcctgagagccatggcgcgcgagcgagccatcct 182
Db 24381 CTGGAGCCACACTGCGCGGCGGTCCGGTCTCGGGCGCTGACCCGCTTCTGACTCCAC 24322
QY 183 gbatcgctgagaaactgacgcgagagagctcaagaagtcaagtcaagtcaagtctgtc 242
Db 24321 CGGTACCGGCGGCGGAGTGGCGGAGGTGAATTCACCGCGGAGAACTCTGCCGG 24262
QY 243 ggtgcgctgcgcgaggtgctacggcgatcccgcggtcccgcggtgctgctccatgagcg 302
Db 24261 CCGACTGTGCGCGAGACCGACACATGACGCGGCTGGCCCTGTGTCGCGCGAGGAGCG 24202
QY 303 cttggaacctaccgacaagtgtgagcttctacgtgagacactagacgagcgagctcac 362
Db 24201 GCTCCCGACGCGGGGCGGACCCGACGACGATGCGGAGTTCGCGCGCGGTCTGTGAC 24142
QY 363 cgttaoagctgctgcgacatgggctgagagatggcgggcgagctgagggcgccac 422
Db 24141 GCGCCGCTCGGCGGCGGTTCAGTTCGGCCAGAGAACTCTCAGGCGCTGTGGAGCAA 24082
QY 423 gacacaggtgagcgcccccttccctccaccctcttctccctccaccacacag 482
Db 24081 GGGCCCGGCTTACGTACGCCCTTACAGTCTTTCGGTGGTTCCTACCGGTCAACACCG 24022

RESULT 6

US-08-476-519-10
; Sequence 10, Application US/08476519
; Patent No. 5750876
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Krohm, Bradley M.
; TITLE OF INVENTION: No. 5750876el Isoamylase Gene, Compositions

; TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
; STREET: 700 Chesterfield Parkway No. 5750876th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,519
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/281902
; FILING DATE: 28-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bonner, Grace L.
; REGISTRATION NUMBER: 32,963
; REFERENCE/DOCKET NUMBER: 38-21(13577)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-7286
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2241
; US-08-476-519-10

Query Match 8.0%; Score 50; DB 1; Length 2244;
Best Local Similarity 44.9%; Pred. No. 0.064;
Matches 230; Conservative 0; Mismatches 280; Indels 2; Gaps 1;
QY 15 gaggggcagcgagcgggcggtgagtcgagagaccagagtgaggagggagggaggtccc 74
Db 1339 GAGTGAACGGCTCTACCCGCGGCTGCGCAAGAACAGCAAGCAAGCTCGGCGTGGAA 1398
QY 75 aggttcgcccgcgagcgagcttctcctctggtcgcggtcgagcggtgagcgcgcg 134
Db 1399 ACGGTACCCCGGCGGCGGCTGGCCGCGCTTCGCGGCTCCACGACCTGTACGGCGAC 1458
QY 135 agcgcgcggtgatcctgg--agccatggggcgcgcgcgagcgaacctctggatgcgctg 192
Db 1459 GAGCGCGCCAGCGCGTGGCATTCGATCAACTTCGTGGTGGCCGACGACGCTTCACCCCTC 1518
QY 193 gagaacctgacccgcgagagagctcaagaagttcaagctgaagctgctgctgctgctg 252
Db 1519 AAGGACCTGTAGCGCTACACGACAGAGAACACAGCCGCTGGCGGTACGGCGCGTCC 1578
QY 253 cgcgagggctacggcgagcaccgcccggggcgcgctgctgtccatggagcgctggacctc 312
Db 1579 GACGGCGCGGAGGACCAACCTGAGCTGGAACACGAGCGGCGATCTGCGCGGAGCAGCG 1638
QY 313 accgacaagctggtcagcttctacgttcgagagcctacggcgcgagctcaaccgctaacgtg 372
Db 1639 AAGGCGCGCGCACCGGACTGGGCTTGTGCTGATGCTCAGCGCGGCTGCCGATGATCACC 1698
QY 373 ctgacgacatgagcctgagagatggcgcgagctgagcgagcgagcgagcgagcgagcg 432
Db 1699 GCGCGGCGAGGCGCTGCCGACCCAGTTTCGCGCAACACACACTACACCTGGATTGCG 1758

[illegible]

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RESULT      9
PCT-US95-09323-1
; Sequence 1, Application PC/TUS9509323
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Isoamylase Gene, Compositions
; TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09323
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/281902
; FILING DATE: 28-JUL-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2334 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-09323-1

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Db 1612 AAGCACTGTAGGCTTACAGCAAGACAGAAACACAGCGGTGGCCGTACGGGGCCGTCC 1671
 Qy 253 cgcgagggctacggcgcattccgcggcgctgtgtctcatgacgccttggacatc 312
 Db 1672 GACGGCGGAGGACCAACACCTGAGCTCGAACCAGGGCGGCATCGTCGCCAGCAGGCG 1731
 Qy 313 acgcacaagcggcgaactctacctggagacctacgcccgcagctcacccgctaactg 372
 Db 1732 AAGCGCGGCGGACGAGACTGGCGTTGCTGATGCTACGCGCGCGGTGCGGATGATCACC 1791
 Qy 373 ctgcgcgacatggcctgcaggagatgcccggcgagctgcaggcgccaccaccaggggt 432
 Db 1792 GCGCGCGAGAGGGCTCGCACCCAGTTCGGCAACAAACACACCTACAACTGGATTTCG 1851
 Qy 433 gagcgcgccccgttccccctcaccccgctcttccccctccaccacaccagcgcttacc 492
 Db 1852 GCGGCAACTGGCTGACTGGAGCGCGAGCGGCTCGAGGCGGACCAACGAGACCTACACC 1911
 Qy 493 gggggcttcgcgtttctgttctctctacc 524
 Db 1912 AAGCGCTGTATCGCGTTTCGCAAGGCGCACCC 1943
 RESULT 10
 US-08-459-586-15
 : Sequence 15, Application US/08459586
 : Patent No. 5720957
 : GENERAL INFORMATION:
 : APPLICANT: Jones, Thomas R.
 : APPLICANT: Campbell, Ann E.
 : TITLE OF INVENTION: Identification of a Human
 : TITLE OF INVENTION: Cytomegalovirus Gene Region Involved in Down-Regulation of
 : TITLE OF INVENTION: MHC Class I Heavy Chain Expression
 : NUMBER OF SEQUENCES: 20
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: American Cyanamid Company
 : STREET: One Campus Drive
 : CITY: Parsippany
 : STATE: New Jersey
 : COUNTRY: United States
 : ZIP: 07054
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/459,586
 : FILING DATE: 02-JUN-1995
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Barnhard, Elizabeth M.
 : REGISTRATION NUMBER: 31,088
 : REFERENCE/DOCKET NUMBER: 32,425-01
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 201-683-2158
 : TELEFAX: 201-683-4117
 : INFORMATION FOR SEQ ID NO: 15:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1765 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 US-08-459-586-15

Db	104	CCTAGCGCGCCCGCGGGCGCGGATTTCGTGCTCTTAACGCGGACGCGCCACGCGGTGG	163
QY	83	cccgcgagcgaacttctctctgctgcgcgctgcagcgggtgagcgcgcgcagcgcgcg	142
Db	164	TGCGGGCGGACGCGCGCAGCAGCAGCGCGCCACCGGTGATGGTGGTTTCACACGCGATGG	223
QY	143	ggatccttgagacatgggggcgcgcgcgcacatcctggatgcgctggagaaactga	202
Db	224	CGGGTCCGCGCGGTGCGGGACCTGCCGCGGCCATGCTGGTGGTCTGCTGGACGAGC	283
QY	203	ccgcgcgagagctcaagaagtctcaagctgaactctgtcgtgcgcctgcgcgcgcgcgcgc	262
Db	284	TGGGGCGCGTGTTCGGGTACTGCCCGCTGGACGGGACAGTGATCCCGCTTGGCGCGGAGC	343
QY	263	acgggcgcattccgc	322
Db	344	TGTCGCATCTTCTGCGCGCGGCGTGTGGCGCGCTGGCGCTGGACGCGAGTCGGCGC	403
QY	323	tggtcaactcttacctgagacctaaaggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	382
Db	404	CCGCGCGGAGCGCGCGGGCGGTGCTGCCCGAGCTGGACCGGAGCAGTGGGAGCGGC	463
QY	383	tgggcctcgcaggagatggccggggcagctgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	441
Db	464	CGCGCTGGAGACGGGTGACCTGCACCGCGCGCGCGCTGTGGCGCGCGCAGCGCGAC	522

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RESULT 11
US-08-283-696-15
: Sequence 15 Application US/08282696
: Patent No 5645806
: GENERAL INFORMATION:
: APPLICANT: Jones, Thomas R.
: APPLICANT: Campbell, Ann E.
: TITLE OF INVENTION: Identification of a Human
: CYTOMEGALOVIRUS Gene Region Involved in Down-Regulation of
: TITLE OF INVENTION: MHC Class I Heavy Chain Expression
:

```

Query Match	7.9%;	Score 49.4;	DB 2;	Length 1765;
Best Local Similarity	44.9%;	Pred. No. 0.083;		

Matches 188; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

QY 23 cggaccgvgggaggatcggggagaccagagtggggaagcgvggagdtccaggttccy 82
DB 104 CGTATCGGCGCCGCCGGGGGCGCATTTGGGTGCTTAACGCGGAGACGGCAGCGGGTGG 163
QY 83 ccccggagccgaactctctcttgctggcggtggaagcgvggtgagcggcgagcggcg 142
DB 164 TCGGGGCGGACGCGGACGAGCAGCGCGCACGGTGATGGTGGTTCGACAGCGATGG 223
QY 143 gggattccitgagaccatggggcgcgcgacgcacctctgatgcgcitggagaacctga 202
DB 224 CCGGTTCGCGGGGTGCGGGAGACGTGCCGCGCCACTGCTGGTGGTGTCTGCTGGAGAGC 283
QY 203 cgccgagagagtcacaagatccaagtcaagctgtctgtcgggtgcgcgcgagggct 262
DB 284 TGSGGCGCGGTGTCGGGTACTTGCACCCTGAGCGGACAGTGTACCCGCTGGCGGCGGAGC 343
QY 263 acggcgcatcccccggggcgctgtctccatgacgccttggacctcaaccgaaagc 322
DB 344 TGTGCACTTTCTGCGCGCGGCTGCTGGCGCGCTGCTGGGACGCGAGTCTGGCGC 403
QY 323 tghtcagttctacctgagacctaacgacgcgcagctcacgcgtacgtgcgcgaca 382
DB 404 CGCCGCGAGCGCGCGCGGCTGCTCCCCGACTGGACCCGCGACAGTAGTGGGAGCGCG 463
QY 383 tgggctcgaggagatgccggcgagctcgagcgggccacgcacccaggttagcgccc 441
DB 464 CGCGTGGGACGCGCTGCACCTGCACCGCGCGCGCGCTGTGGGCGCGGAGCGCGCAC 522

RESULT 12
US-08-459-586-4
Sequence 4, Application US/08459586
Patent No. 5720957
GENERAL INFORMATION:
APPLICANT: Jones, Thomas R.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: Identification of a Human
CYTOMEGALOVIRUS Gene Region Involved in Down-Regulation of
MHC Class I Heavy Chain Expression
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,586
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,425-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 16994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-459-586-4

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Query Match 7.9%; Score 49.4; DB 1; Length 18994;
Best Local Similarity 44.9%; Pred. No. 0.092;
Matches 188; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

QY 23 cggaccgggagggagtcggagaccagagtgaggagagggggggagtcagggttcg 82
Db 14144 CGTACGGCGCCCGCGGGGGGGCGGATTTGGTGCCTAACGGGAGCGGACGGCGGTGG 14203

QY 83 ccccgagccgacttcctctctctctctctctctctctctctctctctctctctct 142
Db 14204 TCGGGCGGAGCGCGGACGAGCAGCGGCGCGGCGGATTTGGTGCCTAACGGGAGCG 14263

QY 143 gggatctggagccatggggcgcgcgcgagccatctctggagtcgagtcgagagcctga 202
Db 14264 CGGGTCCGGCGGCGTGGGAGCGGTCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14323

QY 203 ccgcgagagctcaagaagtccaagtcaagtcaagtcaagtcaagtcaagtcaagtca 262
Db 14324 TGGGCGCGGTGTTCGGGTACTGCGGCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14383

QY 263 acgggcgcatcccgcgggcgcgcgctgtctctctctctctctctctctctctctct 322
Db 14384 TGTGCACTTTCTCGCGCGGCGGCGGCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14443

QY 323 tggtagctttacttgagacctacggcgcgagctcaccgctacgctgctgctcgagaca 382
Db 14444 CCGCGCGGAGGCGCGCGCGCGCGGCGGCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14503

QY 383 tgggctcagagatggcgcgagctgagcgcgagcgcgagcgcgagcgcgagcgcgagc 441
Db 14504 CGCGTGGAGCGCGCTGCACCTGCACCGCGCGCGCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14562

RESULT 13
US-08-282-696-4
; Sequence 4, Application US/08282696
; Patent No. 5848806
; GENERAL INFORMATION:
; APPLICANT: Jones, Thomas R.
; TITLE OF INVENTION: Identification of a Human
; TITLE OF INVENTION: Cytomegalovirus Gene Region Involved in Down-Regulation of
; TITLE OF INVENTION: MHC Class I Heavy Chain Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,696
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,425-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18994 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-282-696-4

Query Match 7.9%; Score 49.4; DB 2; Length 18994;
Best Local Similarity 44.9%; Pred. No. 0.092;
Matches 188; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

QY 23 cggaccgggagggagtcggagaccagagtgaggagagggggggagtcagggttcg 82
Db 14144 CGTACGGCGCCCGCGGGGGGGCGGATTTGGTGCCTAACGGGAGCGGACGGCGGTGG 14203

QY 83 ccccgagccgacttcctctctctctctctctctctctctctctctctctctctct 142
Db 14204 TCGGGCGGAGCGCGGACGAGCAGCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14263

QY 143 gggatctggagccatggggcgcgcgcgagccatctctggagtcgagtcgagagcctga 202
Db 14264 CGGGTCCGGCGGCGTGGGAGCGGTCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14323

QY 203 ccgcgagagctcaagaagtccaagtcaagtcaagtcaagtcaagtcaagtcaagtca 262
Db 14324 TGGGCGCGGTGTTCGGGTACTGCGGCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14383

QY 263 acgggcgcatcccgcgggcgcgcgctgtctctctctctctctctctctctctctct 322
Db 14384 TGTGCACTTTCTCGCGCGGCGGCGGCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14443

QY 323 tggtagctttacttgagacctacggcgcgagctcaccgctacgctgctgctcgagaca 382
Db 14444 CCGCGCGGAGGCGCGCGCGCGCGGCGGCGGCGGCGGCGGATTTGGTGCCTAACGGGAGCG 14503

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RESULT 14
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; Sequence 4, Application US/08758662
; Patent No. 6114150
; GENERAL INFORMATION:
; APPLICANT: Weissman, Sherman
; APPLICANT: Baskaran, Namadev
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 701 Fifth Avenue, 6300 Columbia Center
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,662
; FILING DATE: 29-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6114150tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 390036.402C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2001, 21:14:47 ; Search time 81.93 seconds
(without alignments)
4797.588 Million cell updates/sec

Title: US-09-691-763B-4

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	368	58.8	779	20	Human breast tumou
3	322	51.4	740	22	Human CARD-5 cDNA.
4	320	51.1	432	21	Human colon cancer
5	178.8	28.6	777	22	Mouse CARD-5 cDNA.
6	174.4	27.9	807	22	Human FLEXHT-30 nu
7	86.2	13.8	16891	20	MEFY gene sequence
8	74.8	11.9	3512	20	PMF associated pro
9	68.4	10.9	6461	22	Human ATLAS-2-enco
10	52.6	8.4	44377	18	Platenolide syntha
11	52.6	8.4	44377	18	Platenolide syntha

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c	13	51.2	8.2	2943	17	AAT16480	SA8 virus gB glyco
c	14	50.8	8.1	30001	18	AAT61016	Total DNA sequence
c	15	50.8	8.1	30001	20	AA05110	S. aureofaciens DN
c	16	50.6	8.1	11279	21	AA038389	Pseudomonas sp. WF
c	17	50.6	8.1	53789	19	AAV21187	Amycolatopsis medi
	18	50	8.0	2244	17	AAT10429	Mature isoamylase
	19	50	8.0	2244	19	AAV23640	Flavobacterium iso
	20	50	8.0	2334	17	AAT10428	Isoamylase gene.
	21	50	8.0	2334	19	AAV23639	Full length Flavob
	22	49.4	7.9	1765	20	AAV08427	HCMV strain AD169
	23	49.4	7.9	18994	20	AAV08416	HCMV strain AD169
c	24	48.8	7.8	1925	20	AA090924	Epstein Barr Virus
	25	48.4	7.7	2061	10	AA092408	Sequence encoding
	26	48	7.7	530	21	AA05215	Human OCT-Tl parti
	27	48	7.7	1272	20	AA090910	Brn-3a polynucleot
	28	48	7.7	1272	21	AA029006	Human transcriptio
	29	48	7.7	2310	20	AA021502	Saccharopolyspora
	30	48	7.7	4524	20	AAV33912	Nucleotide sequenc
	31	48	7.7	114955	20	AA053491	Human adenosine A1
	32	47.8	7.6	2538	20	AA021398	Central fragment o
	33	47.4	7.6	2672	16	AAT08693	Cephamycin biosynt
c	34	47.4	7.6	50937	21	AA09469	Streptococcus olea
	35	47	7.5	1844	12	AA012000	Maize nitrite redu
	36	46.6	7.4	1809	17	AAT15008	Mouse Elf-1 cDNA.
	37	46.6	7.4	1809	19	AAV42926	cDNA encoding a ma
c	38	46.6	7.4	15079	16	AAQ91580	S. clavuligerus cl
c	39	46.4	7.4	2106	20	AA028103	Freac11 gene. Hom
c	40	46.2	7.4	861	19	AAV34602	M. vaccae antigen
	41	46.2	7.4	861	20	AA021137	M. vaccae potb gen
	42	46	7.3	1506	20	AA026871	Codon modified cDN
	43	46	7.3	2261	20	AA026865	Cytochrome P450 cD
	44	45.8	7.3	1803	21	AA022389	Human secreted pro
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ALIGNMENTS

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ID AAC77884 standard; cDNA; 811 BP.
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AAC77884;
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08-FEB-2001 (first entry)
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Human cancer associated gene sequence SEQ ID NO:278.
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Human; cancer associated gene; cancer antigen; detection; cancer;
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diagnosis; cytostatic; proliferative; vulnery; immunomodulator;
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antidiabetic; antialthmatic; antirheumatic; antialthritic; antiviral;
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antiflammatory; antihyroid; antiallergic; antibacterial; cardiac;
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dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
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allergic reaction; haematopoietic cell disorder; autoimmune disorder;
XX
haemostatic; thrombolytic; cardiovascular disorder; infection;
XX
neurological disease; drug screening; ss.
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Homo sapiens.
XX
WO2000055350-A1.
XX
21-SEP-2000.
XX
08-MAR-2000; 2000WO-US05882.
XX
12-MAR-1999; 99US-0124270.
XX
(HUMA-) HUMAN GENOME SCI INC.
XX
Rosen CA, Ruben SM;
PI

RESULT 3
 AAF30007
 ID AAF30007 standard; cDNA; 740 BP.
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 AC AAF30007;
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 DT 23-APR-2001 (first entry)
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 DE Human CARD-5 cDNA.
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 KW autoimmune disease; neurological disease; haematological disease;
 KW immune disease; inflammation; antitumour; antiseptic;
 KW immunomodulator; antiinflammatory; apoptosis; diagnosis;
 KW gene therapy; ss.
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 PF 28-JUN-2000; 2000WO-US17691.
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 PR 28-JUN-1999; 99US-0340620.
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 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PT Bertin J;
 XX
 DR WPI; 2001-061973/07.
 DR P-PSDB; AAB20085.
 XX
 PT Isolated intracellular proteins predicted to be involved in regulating
 PT caspase activation are used for diagnosis and treatment of e.g. cancer,
 PT viral infections, autoimmune diseases, neurological diseases and
 PT haematological disorders -
 XX
 PS Claim 1(a): Fig 21; 208pp; English.
 XX
 CC The present sequence is that of cDNA encoding human caspase
 CC recruitment domain 5 (CARD-5, see AAB20085). The cDNA was isolated
 CC from a testis cDNA library using murine CARD-L. Plasmid BpHC5
 CC containing CARD-5 cDNA is deposited as ATCC PTA-213. CARD-5
 CC is an intracellular protein predicted to be involved in regulating
 CC caspase activation. It is useful as a modulating agent in
 CC regulating cellular processes include cell growth and cell death.
 CC Methods of diagnosing and treating patients suffering from a
 CC disorder associated with an abnormal level or rate of apoptotic
 CC cell death, abnormal activity of the Fas/APO-1 receptor complex,
 CC abnormal activity of the tumour necrosis factor receptor complex
 CC or abnormal activity of a caspase involve administering a compound
 CC that modulates the expression or activity of CARD-3, CARD-4, CARD-5
 CC or CARD-6 e.g. a small molecule, antisense nucleic acid, ribozyme
 CC or polypeptide. Such disorders include cancer, viral infection,
 CC autoimmune disorders, neurological diseases, haematological
 CC disorders, inflammatory disorders and immune disorders. CARD
 CC nucleic acids can be used to express CARD proteins in a host cell
 CC e.g. for gene therapy applications, to detect a genetic lesion and
 CC to modulate CARD activity.
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 SQ Sequence 740 BP; 146 A; 238 C; 236 G; 120 T; 0 other;
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 Query Match 51.4%; Score 322; DB 22; Length 740;
 Best Local Similarity 100.0%; Pred. No. 8.7e-50;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 AC AAC98638;
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 DT 09-MAR-2001 (first entry)
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 DE Human colon cancer antigen nucleotide sequence SEQ ID NO:648.
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 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnery;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antineoplastic; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder; ss.
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 OS Homo sapiens.
 XX
 PN WO200055351-A1.
 XX
 PD 21-SEP-2000.
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 PF 08-MAR-2000; 2000WO-US05883.
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 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-587534/55.
 DR P-PSDB; AAB53881.
 XX
 PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -
 XX
 PS Claim 1; Page 1175; 2104pp; English.
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 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnery, nephrotropic, antineoplastic, antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,


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RESULT 10
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 ID AAT78508 standard; DNA: 44377 BP.

XX AAT78508;

DT 26-FEB-1998 (first entry)

DE Platenolide synthase gene cluster..

XX Platenolide synthase gene cluster; platenolide production; srmG gene;
 KW multi-functional protein; macrolide antibiotic; spiramycin; ss.
 XX Streptomyces ambofaciens.

PH Key Location/Qualifiers
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PN EP791656-A2.

XX 27-AUG-1997.

XX 19-FEB-1997; 97EP-0301066.

XX 22-FEB-1996; 96US-0012050.

XX (ELIL) LILLY & CO ELI.

PI Burgett SG, Kuhstoss SA, Rao RN, Richardson MA;
 PI Rosteck PR;

XX WPI: 1997-418047/39.

DR P-PSDB; AAW23716-W23720.

XX DNA encoding Streptomyces ambofaciens platenolide synthase domain -
 PT for production of spiramycin-related polyketide antibiotics

XX Claim 9; Pages 8-33; 8lpp; English.

XX This sequence represents the platenolide synthase gene cluster of the
 CC invention. This sequence is referred to as the srmG gene, and was
 CC isolated from Streptomyces ambofaciens. This sequence encodes the
 CC multi-functional proteins which direct the synthesis of the polyketide

CC platenolide. Platenolide is the basic building block of the macrolide
 CC antibiotic spiramycin. The DNA can be used to produce compounds
 CC exhibiting antibiotic activity based on the platenolide structure,
 CC including specifically the macrolide antibiotic spiramycin and spiramycin
 CC analogues and derivatives. Modifications of the platenolide synthase DNA
 CC sequence can be made so as to change the number and type of carboxylic
 CC acids incorporated into the growing polyketide chain and to change the
 CC kind of post-condensation processing that is conducted.

XX Sequence 44377 BP; 4965 A; 15552 C; 17381 G; 6479 T; 0 other;

Query Match 8.4%; Score 52.6; DB 18; Length 44377;
 Best Local Similarity 55.9%; Pred. No. 0.15;
 Matches 100; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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RESULT 11

AAT80414
 ID AAT80414 standard; DNA: 44377 BP.

XX AAT80414;

DT 27-FEB-1998 (first entry)

DE Platenolide synthase gene cluster.

XX Tyactone synthase gene cluster; tylG gene; multifunctional protein;
 KW platenolide synthase gene cluster; platenolide production; srmG gene;
 KW polyketide; tyactone synthesis; antibiotic; tylosin; ss.

OS Streptomyces ambofaciens.

PH Key Location/Qualifiers
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 FT /note= "ORF2 encodes protein shown in AAW22607"
 CDS 20110..31284
 FT /*tag= c
 FT /transl_except= (pos:20111..20113, aa:Met)
 FT /note= "ORF3 encodes protein shown in AAW22608"
 CDS 31329..36071
 FT /*tag= d
 FT /note= "ORF4 encodes protein shown in AAW22609"
 CDS 36155..41830
 FT /*tag= e
 FT /note= "ORF5 encodes protein shown in AAW22610"

PN EP791655-A2.

XX 27-AUG-1997.

XX 19-FEB-1997; 97EP-0301056.

XX 22-FEB-1996; 96US-0012078.

XX (ELIL) LILLY & CO ELI.

```

XX Dehoff BS, Kuhstoss SA, Rostock PR, Sutton KL;
PI WPI; 1997-418046/39.
XX P-PSDB; AAW22606-W22610.
DR DNA encoding Streptomyces fradiae tyllactone synthase domain - for
XX production of tyllactone-related polyketide compounds
XX Example 2; Pages 110-134; 220pp; English.
XX
CC This sequence represents the platenolide synthase gene cluster of the
CC invention. This sequence is referred to as the smg gene, and was
CC isolated from Streptomyces ambofaciens. This sequence encodes the
CC multi-functional proteins which direct the synthesis of the polyketide
CC platenolide. Platenolide is the basic building block of the macrolide
CC antibiotic spiramycin. This sequence was used along with the tylg gene
CC (see AAT80413) to create a hybrid ORF1 sequence (see AAT80415). The tylg
CC gene is the tyllactone synthase gene cluster of the invention. The tylg
CC sequence was isolated from Streptomyces fradiae, and encodes
CC multifunctional proteins which direct the synthesis of the polyketide
CC tyllactone. Tyllactone is the basic building block of the antibiotic
CC tylosin. The hybrid sequence can be used to transform S. ambofaciens
CC lacking the smg ORF1 sequence, or S. fradiae lacking the tylg ORF1
CC sequence, so that they can produce polyketides. The DNA sequence can be
CC modified so as to alter the type of carboxylic acids incorporated, the
CC number of carboxylic acids incorporated and/or the post-condensation
CC reactions performed, thereby resulting in novel tylosin-related
CC polyketides.
XX
SQ Sequence 44377 BP; 4965 A; 15552 C; 17381 G; 6479 T; 0 other;

Query Match      8.4%; Score 52.6; DB 18; Length 44377;
Best Local Similarity 55.9%; Pred. No. 0.15;
Matches 100; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Oy 329 gctctacgtgagactacgagcgccgagctcaccgtaacgtgctcgcgacatgggcc 388
   || || || || || || || || || || || || || || || || || || || ||
Db 16843 gcatcagctcccaactacccttccacacgacgctactggtggtggtggtcc 16902

Oy 389 tgcagagatggcggcgagctcagcgccgacacgacgaggtgagccgcccccttcc 448
   || || || || || || || || || || || || || || || || || || || ||
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Oy 449 cctccacccgctcttccctccacacacacgagcgttacccggtggtcttccgct 507
   || || || || || || || || || || || || || || || || || || || ||
Db 16963 cgccgctggaactcccgccgacacgacgaggtgtggtggtggtggtggtggt 17021

RESULT 12
AA11992/c
ID AA11992 standard; DNA; 37856 BP.
XX
XX AA11992;
XX
XX 07-AUG-2000 (first entry)
XX
XX S. cellulosum DNA encoding polyketide and heteropolyketide enzymes.
XX
XX Polyketide biosynthesis; heteropolyketide biosynthesis; mutasynthesis;
KW epothilone; cytotoxic; immunosuppressant; antibiotic; antifungal;
KW plant-protection; ds.
XX
XX Sorangium cellulosum.
XX
XX Key Location/Qualifiers
XX Key complement (3398..6100)
XX CDS /*tag= a
XX /*product= "ORF1-trna synthetase"
XX /*note= "gtg start codon"
XX /*complement (6374..7111)
XX /*tag= b
XX

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FT 9855..11393
FT /*tag= d
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FT /note= "GTG start codon"
FT 12212..13658
FT /*tag= e
FT /product= "ORF5-3-oxoacyl-ACP-reductase"
FT /note= "ACC start codon"
FT 15374..19984
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FT /*tag= g
FT /product= "ORF7-peptide synthetase"
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FT /*tag= h
FT /product= "ORF8-transpeptidase"
FT complement (30040..31720)
FT /*tag= i
FT /product= "ORF9-regulation element"
FT /note= "CGC stop codon"
FT 31982..32932
FT /*tag= j
FT /product= "ORF10-transcription regulator"
FT 33128..33613
FT /*tag= k
FT /product= "ORF11-regulation element"
FT /note= "GTG start codon"
FT 33661..34077
FT /*tag= l
FT /product= "ORF12-regulation element"
FT complement (35255..35616)
FT /*tag= m
FT /product= "ORF13-transcription regulator"
FT complement (35730..36242)
FT /*tag= n
FT /product= "ORF14-transcription regulator"
FT /note= "GTG start codon"
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XX DE19846493-A1.
XX
XX 13-APR-2000.
XX
XX 09-OCT-1998; 98DE-1046493.
XX
XX 09-OCT-1998; 98DE-1046493.
XX
XX (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
XX Beyer S, Mueller R;
XX
XX WPI; 2000-294101/26.
XX
XX DNA sequence coding for products involved in the biosynthesis of
XX polyketide or heteropolyketide compounds, especially epothilone
XX Claim 3; Page 20-33; 36pp; German.
XX
XX This invention describes a novel DNA sequence (I) whose expression
XX products effect or are involved in the enzymatic biosynthesis,
XX mutasynthesis or partial synthesis of polyketide or heteropolyketide
XX compounds (II). (I) can be inserted into an expression vector and used
XX to transform or transfect prokaryotic or eukaryotic cells with the aim
XX of obtaining strains that produce large amounts of polyketide or
XX heteropolyketide compounds, especially epothilones, which have cytotoxic
XX and/or immunosuppressant and antibiotic and antifungal activities and
XX are useful as plant-protection agents. This sequence represents the DNA
XX sequence isolated from Sorangium cellulosum which is described in the

```


XX	DE	Total DNA sequence from cosmid clones LP(2)127 and LP(2)128.	
XX	XX	Cosmid clone; LP(2)127; LP(2)128; chlortetracycline;	
KW	KW	biosynthetic pathway; recombinant; production; antibiotic;	
KW	KW	heterologous host; Streptomyces lividans; ss.	
XX	OS	Streptomyces aureofaciens.	
XX	XX	US5589385-A.	
XX	XX	31-DEC-1996.	
XX	XX	26-JUL-1990; 90US-0558039.	
XX	XX	22-SEP-1993; 93US-0125468.	
PR	PR	26-JUL-1990; 90US-0558039.	
PR	PR	26-JUL-1990; 90US-0558040.	
PR	PR	15-JAN-1992; 92US-0821109.	
PR	PR	15-JAN-1992; 92US-0821419.	
XX	PA	(AMCY) AMERICAN CYANAMID CO.	
XX	XX	Fantini SE, Lotvin JA, Ryan MJ, Strathy N;	
XX	XX	WPI; 1997-076853/07.	
XX	XX	DNA encoding tetracycline biosynthetic pathway proteins -	
PT	PT	specifically from Streptomyces aureofaciens for expression in	
PT	PT	heterologous hosts, specifically S. lividans	
XX	XX	Claim 3; Columns 17-44; 39pp; English.	
XX	XX	The present sequence is the total DNA sequence from cosmid clones	
CC	CC	LP(2)127 and LP(2)128, which contains a Streptomyces aureofaciens	
CC	CC	(ATCC 13899) DNA that encodes the proteins of the entire	
CC	CC	chlortetracycline biosynthetic pathway. The biosynthetic gene,	
CC	CC	which can be expressed in heterologous hosts, especially	
CC	CC	S. lividans, may be useful in the production of antibiotics.	
XX	XX	Sequence 30001 BP; 4055 A; 10939 C; 11019 G; 3988 T; 0 other;	
SQ	SQ		
Query Match	8.1%;	Score 50.8;	DB 18; Length 30001;
Best Local Similarity	45.6%;	Pred. No. 0.32;	
Matches 219;	Conservative	0;	Mismatches 257; Indels 4; Gaps 1;
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Db	24497	CGGCGCTTCAGACGGCGATGCTGCTGCGCGAGCGGAGTGGAGCCGGGATACCGAC	24438
QY	63	ggcggggagtcaggttcgcccccggagccgaacttctctctggtcgggcggtcgagcg99	122
Db	24437	GTCGTGTGACCGGATCGGC-----GTGGTGGCAGCGAAGCGGTGGGCGGTGGCGAGTA	24382
QY	123	gtaagcgcgagcgagcggggatccttgagccatggggcgcgcgcgagccatcct	182
Db	24381	CTGGACCCACACTGGGGCGCGGTCCGGTCTCGGGCGCTGACCCGCTTCGACTCCAC	24322
QY	183	ggatcgctgtgagaacctgaocgcgagagagctcaagaagttcaagctgaagctgtctc	242
Db	24321	CGGGTACCGGGCGACGTGGCGCGAGGTGAACTTTCACGCCGGAGAACACCTTGGCGGG	24262
QY	243	ggtccgctgcgagagctacggcgcatcccgcgggcgcgctgctgtccatggagc	302
Db	24261	CGGACTGCTCCCGACACGACACATGACCGCGGTGGCCCTTGTCGGCGCGAGGAGC	24202
QY	303	cttgagacctaccgacaagctggttcagcttctaccttgagacctacggcgccgagctcac	362
Db	24201	GCTCGCGACGCGGGGCGGACCCGACGACGATGCGCGACTTCTCCGCGCGCTGCTGAC	24142
QY	363	cgctaaagtctgcgacatggccttcagagagatggccgggagctgcagggcgccac	422

Qy 3 cgccctttgctgaggggcaacgagccggggcgaggagtcgaggagaccagagtgaggagaa 62
 Db 24497 CGGCGGCTTCCAGAGCGCGATCGTGCAGCGCGAGTCGAGCGGGGATGACCGAC 24438
 Qy 63 ggcgggagtcagggtccgcccgcgagccgacttcctcctggtcggcggtgcaagcggg 122
 Db 24437 GTCTGTGTACCGGATCGGC---GTGGTGACCGAACCGCTGGGGCTTCGGAGTA 24382
 Qy 123 gtgagcgcgcgagcgccggggtatcctgtgagccatgggcgcgcgagcgccatcct 182
 Db 24381 CTGGGACGCCACACTGGCGGCGGCTCCGGTCTCGGGCGCTGACCGCTTCGACTCCAC 24322
 Qy 183 gaatgcgctgagaaacctgaccgagagctcaagaagttcaagctaaagctactgtc 242
 Db 24321 CCGGTACCGGCGCACGTGGCGCGGAGGTGAACCTACGCGGAGGACACCTGCCGG 24262
 Qy 243 ggtgcgctgaggggtacggcgcatcccgcgggcgcgctgctgtccatggaagc 302
 Db 24261 CCGACTGTGTGCGGAGACCGACACATGACGCGGCTGGCTCGCGGCGGAGGAGC 24202
 Qy 303 cttggacctcaccgacaaagctggtcagcttctaacctgagagacctacggcgcgagctcac 362
 Db 24201 GCTCGCGGACGCGGGGCGGACCGGACGAGATGCCGACTTCTCCGCGGCGTGTGAC 24142
 Qy 363 cgctaactgtgcgacatatgggacctgcaggagatggcgggcgagctgcagcgggccac 422
 Db 24141 GCGCGCTCGGCGCGGCTTCGAGTTCGGCCAGAAAGAACTCCAGGCGCTGTGGAGCAA 24082
 Qy 423 gcaccagggtgagccgcccccggtcccccctccaccocgctcttcccccaccaccacacag 482
 Db 24081 GGGCCCGGCTACGTCAGCGCCTACCACTCCTTCGCGTGTCTACCCCGGTCAACACCGG 24022

Search completed: August 30, 2001, 22:32:50
 Job time: 4683 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2001, 20:41:57 ; Search time 1242.53 Seconds
(without alignments)
7792.819 Million cell updates/sec

Title: US-09-691-763B-4

Perfect score: 626

Sequence: 1 agcgcttttctgtgagggc.....ggaagggaaggatcactt 626

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
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8: gb_ov.*
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10: gb_pat2.*
11: gb_ph.*
12: gb_pl1.*
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14: gb_pl3.*
15: gb_pl4.*
16: em_ba1.*
17: em_ba2.*
18: em_fun.*
19: em_htgo_hum.*
20: em_htgo_inv.*
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25: em_htg_hum4.*
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27: em_htg_hum6.*
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94: gb_pl1.*
95: gb_pl2.*
96: gb_pl4.*
97: gb_pl10.*
98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	626	100.0	2821	89	AF184072	Homo sapi
2	626	100.0	233425	60	AC009088	Homo sapi
3	368	58.8	779	9	AX017270	Sequence
4	361	57.7	782	85	AB023416	Homo sapi
5	342.8	54.8	713	89	AF255794	Homo sapi
6	342.6	54.7	770	89	AF184073	Homo sapi
7	322	51.4	740	10	AX082246	Sequence
8	301	48.1	740	89	AK000211	Homo sapi


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Db 1280 CTGGATCGCTGGAGAACCTGACCGCGAGGAGCTCAAGAGATTCAAGCTCAAGCTGCTG 1339
Qy 241 tgggtgccctcgagggctacggcgcatcccgcgagggcgagctgctccatggac 300
|||||
Db 1340 TCGGTGCCCTCGCGAGGGCTACGGGCGATCCCGGGGGCGCTGCTGTCCATGGAC 1399
Qy 301 gcttggacctcacgacaagtggctcagcttctaccttgagacctagcgcgagctc 360
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Db 1400 GCCTTGGACCTCACGACAAGCTGGTCAGCTTCTACCTTGAGAGACTACGGCGCGAGCTC 1459
Qy 361 accgctaacgtgctcgacatggcctcagagatgagcggcgagctgcagcgagcc 420
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Db 1460 ACCGTAACGTGCTGGCGACATGGGCTTCAGAGATGGCGGGGAGCTGACAGCGGCC 1519
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Db 1520 ACGCACAGGGGTGAGCGCGCCCGCTTCCCTCCACCCGCTCTTCCCTCCACCCACAC 1579
Qy 481 agcgttaccgcggggtcttccgctttctgcttctctaccctaccctaaacaaagctgctc 540
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Db 1580 AGCGTTACCCCGGGGCTCTCCGCTTTCTGTTCTCTCTACCCCTAAACAAGCTGCTC 1639
Qy 541 taccggaaggaggtcccccagcttggtctaccgacacaaagggagcccccagcgcc 600
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Qy 601 gggagggagggagggggtacactt 626
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Db 1700 GGGAAGGAAGGAGGAGGATCACTT 1725

RESULT 2
AC009088
LOCUS Homo sapiens chromosome 16 clone RP11-388M20, WORKING DRAFT
DEFINITION AC009088
ACCESSION AC009088
VERSION AC009088.5 GI:9256130
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 233425)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 233425)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:7689912.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 555665
Center clone name: RPCI-11_388M20
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Summary Statistics
Consensus quality: 221761 bases at least Q40
Consensus quality: 229603 bases at least Q30
Consensus quality: 231140 bases at least Q20
Estimated insert size: 252540; agarose-fp estimation
Estimated insert size: 235025; sum-of-ctnigs estimation
Quality coverage: 7.01 in Q20 bases; agarose-fp estimation
Quality coverage: 7.6 in Q20 bases; sum-of-ctnigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
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* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 37667: contig of 37667 bp in length
* 37668 37667: gap of unknown length
* 37669 64793: contig of 27026 bp in length
* 64794 64893: gap of unknown length
* 64894 96964: contig of 32071 bp in length
* 96965 97064: gap of unknown length
* 97065 119624: contig of 22560 bp in length
* 119625 119724: gap of unknown length
* 119725 155221: contig of 35797 bp in length
* 155222 155621: gap of unknown length
* 155622 175096: contig of 19475 bp in length
* 175097 175197: gap of unknown length
* 175198 175984: contig of 788 bp in length
* 175985 176084: gap of unknown length
* 176085 208395: contig of 32311 bp in length
* 208396 208495: gap of unknown length
* 208496 223734: contig of 15239 bp in length
* 223735 223834: gap of unknown length
* 223835 233425: contig of 9591 bp in length.
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Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 10930 AAGCGGGGAGTCCAGGTTCCGCCCGGAGCCGACTTCTCTCTGCTCGCGGCTCGACGC 10989
Qy 121 gggtagcgcgacgacggcgagggatcttgagcagcagtcggggcgcgcgagccacatc 180
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Qy 481 agcgcttaccgcggggtcttccgctttctgcttctctaccctaccctaaacaaagctgctc 540
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Db 241 ATGGCGGGGAGCTGCAGGGCGGCGCAGCAGGAG 275

RESULT 11
LOCUS BC004470 768 bp mRNA PRI 14-MAR-2001
DEFINITION Homo sapiens, clone MGC:10332, mRNA, complete cds.
ACCESSION BC004470
VERSION BC004470.1 GI:13325315
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 768)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbio.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 14 Row: g Column: 9.
Location/Qualifiers
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BASE COUNT 168 a 229 c 256 g 115 t
ORIGIN

Query Match 37.1%; Score 232.4; DB 91; Length 768;
Best Local Similarity 99.6%; Pred. No. 2.3e-24;
Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 agcgcttttctggaggcaacgagccggcgaggagtcgggagaccagagtgagg 60
Db 90 AGCGCTTTTCTGGAGGACACGACCGCGGGAGTGGGAGACCAAGAGTGGGAG 149
Qy 61 aaqcgggggagtcagattcccccggagccgacttcctcctggtcgagctcagcg 120
Db 150 AAGCGGGGAGTCCAGGTTCCGCCCGGAGCGGACTTCTCTCTGTCGGCGCTCCAGG 209
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Qy 121 gggtagcgccgagcgagccggggggtatcctctggagccatggggcgcgcgagccatc 180
Db 210 GGGTAGCGCGGCGAGCGCGGGGATCTTGGAGCCATGGGCGCGCGCGAGCCATC 269
Qy 181 ctgtagctgtagagaaactgacccgaggaactcaagaattcaagctgaag 234
Db 270 CTGGATGCGCTGGAGAACTGACCGCGGAGAGCTCAAGAGTTCAAGCTGCAG 323

RESULT 12
AX082258
LOCUS AX082258 777 bp DNA PAT 27-FEB-2001
DEFINITION Sequence 60 from Patent WO0100826.
ACCESSION AX082258
VERSION AX082258.1 GI:13171016
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 777)
AUTHORS Bertin, J.
TITLE Novel molecules of the card-related protein family and uses thereof
JOURNAL Patent: WO 0100826-A 60 04-JAN-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
1. .777
/organism="Mus musculus"
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89. .670
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/codon_start=1
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LQMDAILDTKLVSYYLESYGLEMTVLRDMQLQELAEOLQTTREESGAVAAASVP
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BASE COUNT 212 a 193 c 217 g 155 t
ORIGIN

Query Match 28.6%; Score 178.8; DB 10; Length 777;
Best Local Similarity 70.9%; Pred. No. 9.9e-17;
Matches 251; Conservative 0; Mismatches 102; Indels 1; Gaps 1;

Qy 81 cgccccgagcgagcttctctctctctctctctctctctctctctctctctctctct 139
Db 12 CGTCCGGCAGCAGCGAGGCTGCAGAGCGCGAGCAGCAGCAAGAGTAAAGGTGACC 71
Qy 140 ccggggatcttgagccatggcgcgcgcgagccctctctctctctctctctctctct 199
Db 72 CTGCCCCACCCAGAGCCATGGGGGGGCGGACGAGATGCCATCCTTGGAAACT 131
Qy 200 tgacccgagagagctcaagaagttcaagctgaagctcgtctcgttccgctcgcgagg 259
Db 132 TGTCAAGGGATGAACCTCAAAAGTTCAAGATGAAGCTGCTGCACAGTCAACTGCG 191
Qy 260 gctacgggcgcatcccgcgcgcgctgctgtccatggagccttgacctcaccgaca 319
Db 192 GCTATGGCGCATCCACGCGGGGCCCTGCTGCAGATGGAGCCATAGATCTCACTG 251
Qy 320 agctggtcagcttctactgagacctacgagccgagccagctcaccgctaaagctcg 379
Db 252 AACTTGTACGCTACTACTCTGAGTCTGTATGGCTTGTGCTTCACTCACTGCTTAG 311
Qy 380 acatgggctcaggagatggcgggcgagctgcagtcgagcgccaccacccaggg 433
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RESULT 13
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[illegible]

LOCUS HUMZD54H05 556 bp mRNA PRI 29-AUG-1998
DEFINITION Homo sapiens full length insert cDNA clone ZD54H05.
ACCESSION AF086332
VERSION AF086332.1 GI:3483677
KEYWORDS FLI.CDNA.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 556)
AUTHORS Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
Walth,G., Bowles,L., Wylie,T., Bowers,Y., Septoe,M., Theising,B.,
Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L.,
Wilson,R. and Waterston,R.
TITLE Full Clone Sequencing of the Longest Available Member from Each
Unigene Cluster
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 556)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

The location of this clone is unknown.

FEATURES
Source Location/Qualifiers
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ORIGIN

Query Match 27.9%; Score 174.4; DB 97; Length 556;
Best Local Similarity 77.6%; Pred.No.4.9e-16;
Matches 211; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
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Db 121 AGCTCAAGAAGTCAAGTGAAGCTGGGACGGTCCCTGCCGCGAGGGCTTGGAGCGCA 180
QY 272 tcccgcgggcgcgctgctgcattgagacgcttgacctaacccagaagctggtcagct 331
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Db 181 TCCCGCGGGGCGCGCTCGGGCAGCTAGATATCGTGGACCTCACCAGCAAGCTGTCGCT 240
QY 332 tctactgagacacacgagcgagcagctcacgctaacgtgctgcgacatggcctgc 391
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Db 241 CCTACTACGAGGACTACCGACCGAGCTGCTGCTGGCCGCTGCTGGCGACATGCGCATGT 300
QY 392 aggagatggccgggcagctgcagcgccacg 423
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Db 301 TGCAGGAGGCCGCGACGGCTGCGAGGGGCTGCG 332

Search completed: August 30, 2001, 22:30:38
Job time: 6521 sec

